

REMARKS

Reconsideration and allowance are respectfully requested.

Claims 34-42 and 46 are pending in the application with Claim 34 being the sole independent claim.

Applicants respectfully request a signed copy of the IDS submitted April 27, 2001 for their files.

Turning to the Office Action mailed December 19, 2003:

Claims 34-42, and 46 have been rejected under **35 U.S.C. § 101** and **35 U.S.C. §112, first paragraph**. Applicants respectfully traverse. Applicants respectfully submit that there is no reason to doubt that the amino acid sequence of SEQ ID NO:6 has 3-dehydroquinase synthase activity, based on percent identity to a reference protein. Regardless, see also the attached Appendix A. Appendix A corresponds to the first page of a BLASTP analysis performed June 7, 1999, using the amino acid sequence derived from clone se3.pk0029.f9: fis1 (SEQ ID NO:6) as a query against the NCBI database. Furthermore, two specific and substantial utilities for the polypeptides of the invention are described in the specification at page 10, lines 26-30 and page 1, lines 18 and 19.

Claims 34-42, and 46 have been rejected under **35 U.S.C. §112, first paragraph**, as allegedly not being enabled. Applicants respectfully traverse.

Applicants previous remarks in the response filed February 26, 2003 are incorporated here again.

One of ordinary skill in the art can combine the specification with the teachings of both Bischoff et al. and of Carpenter et al., which Applicants submit are within the knowledge of one of ordinary skill in the art, to determine polynucleotides encoding a polypeptide having 3-dehydroquinase synthase activity, wherein the amino acid sequence of the polypeptide is at least 90% identical to the amino acid sequence having SEQ ID NO:6. Bischoff et al. demonstrated that an *L. esculentum* 3-dehydroquinase synthase was capable of complementing a strain of *E. coli* that is deficient in such enzyme, even though the *E. coli* 3-dehydroquinase synthase is only 52.2% identical to the *L. esculentum* enzyme. Carpenter et al. teach nine key amino acids involved in critical interactions in the proposed 3-dehydroquinase synthase catalytic mechanism. One of ordinary skill in the art, in view of both of these teachings, can identify which amino acids can and cannot be changed in an amino acid sequence having at least 90% identity to SEQ ID NO:6, while still retaining 3-dehydroquinase synthase activity.

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Applicants believe the foregoing to be responsive to each of the points raised in the Office Action. Early and favorable notification of allowance is hereby solicited.

Please charge any fees associated with the filing of this response, including but not limited to the Extension of Time, to Deposit Account No. 04-1928 (E. I. du Pont the Nemours and Company). If the fee is insufficient or incorrect, please charge or credit the balance to the above-identified deposit account.

Respectfully submitted,



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APPENDIX A

BLASTP 2.0.8 [Jan-05-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= se3.pk0029.f9.fis1
(437 letters)

6/7/99 no filter, Becky

Database: /blast/data/2.0/2/nr
380,262 sequences; 116,472,368 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value	pLog
gi 114181 sp P07639 AROB_ECOLI 3-DEHYDROQUINATE SYNTHASE >gi 683...	368	e-101	101.00
gi 3023329 sp P77980 AROB_SALTY 3-DEHYDROQUINATE SYNTHASE >gi 16...	363	1e-99	
gi 1168503 sp P43879 AROB_HAEIN 3-DEHYDROQUINATE SYNTHASE >gi 10...	349	2e-95	
gi 3913105 sp O50468 AROB_NEIGO 3-DEHYDROQUINATE SYNTHASE >gi 26...	348	4e-95	
gi 3913106 sp P73997 AROB_SYNY3 3-DEHYDROQUINATE SYNTHASE >gi 16...	272	5e-72	
gi 399057 sp P31102 AROB_BACSU 3-DEHYDROQUINATE SYNTHASE >gi 143...	238	6e-62	
gi 2492962 sp P56081 AROB_HELPY 3-DEHYDROQUINATE SYNTHASE >gi 23...	211	9e-54	
gi 98800 pir S17768 3-dehydroquinase synthase (EC 4.6.1.3) - My...	210	2e-53	
gi 3915615 sp P36919 AROB_MYCTU 3-DEHYDROQUINATE SYNTHASE >gi 17...	210	2e-53	
gi 4154792 (AE001464) 3-DEHYDROQUINATE SYNTHASE (Helicobacter py...	208	5e-53	

>gi|114181|sp|P07639|AROB_ECOLI 3-DEHYDROQUINATE SYNTHASE >gi|68385|pir||SYEQ 3-dehydroquinase

synthase (EC 4.6.1.3) - Escherichia coli
>gi|40968|emb|CAA27495| (X03867) 3-dehydroquinase
synthase (aa 1-362) [Escherichia coli]
>gi|41225|emb|CAA79666| (Z19601) ORF, aroB. Millar G.,
Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia
coli] >gi|606323 (U18997) 3-dehydroquinase synthase
[Escherichia coli] >gi|1789791 (AE000414)
3-dehydroquinase synthase [Escherichia coli]
Length = 362

Score = 368 bits (935), Expect = e-101
Identities = 191/333 (57%), Positives = 234/333 (69%), Gaps = 2/333 (0%)

Query: 76 VEVDLGSRYSYPIYIGSGLLNQPDYLQRHVHGKRVLVVTNETVAPLYLDKVVLDALTRGNPN 135
+ V LG RSYPI I SGL N+P G++V++VTNET+APLYLDKV L +
Sbjct: 4 IVVTLGERSYPITIASGLFNEPASFLPLKSQGEVMLVTNETLAPLYLDKVRGVLEQAG-- 61

Query: 136 VSVESVILPDGEQYKMDTLMKVFDKAIERSRLDRRCTFVALGGGVIGDMCGFAASAFLRG 195
V+V+SVILPDGEQYK + L VF ++ R T VALGGGV+GD+ GFAA+++ RG
Sbjct: 62 VNVDSVILPDGEQYKSLAVLDTVFTALLQKPHGRDTTLVALGGGVVGDLTGFAAASYQRG 121

Query: 196 VNFIIQIPTTVMAQVDSSVGGKTGINHRLGKNMIGTFYQPCVLIDTDTLNLTPDRELASG 255
V FIQ+PTT+++QVDSSVGGKT +NH LGKNMIG FYQP V++D D L TLP RELASG
Sbjct: 122 VRFIQVPTTLLSQVDSSVGGKTAVNHLPLGKNMIGAFYQPASVVVDLCLKTLPPRELASG 181

Query: 256 LAEVIKYGLIRDAEFFEWQEKNMHLLARDPSVMAYAIRKSCENKAEEVVSLDQKESGLRA 315
LAEVIKYG+I D FF W E+N+ LL D MAY I+R CE KAEVV+ D++E+GLRA
Sbjct: 182 LAEVIKYGIILDGAFFNWLEENLDALLRLDGPAMAYCIRRCCELKAEVVAADERETGLRA 241

Query: 316 TLNLGHTFGHAIETGVGYGQWLHGEAVAAGTVMVAVDMSYRLGWIDDSLVKRVGDILKQAK 375
LNLGHTFGHAI E +GYG WLHGEAVAAG VMA S RLG + +R+ +LK+A
Sbjct: 242 LLNLGHTFGHAI EAEMGYGNWLHGEAVAAGMVMAARTSERLGQFSSAETQRIITLLKRA 301

Query: 376 LPTAPPETVTVD MFKSVMAVDKKVADGLRLIL 408
LP P ++ + M DKKV G +RLIL
Sbjct: 302 LPVNGPREMSAQAYLPHMLRDKKVLAGEMRLIL 334